In the Claims

1-41 (canceled).

42. A composition of matter comprising:

a) an isolated polypeptide having chemotactic activity selected from the group consisting of:

1) the amino acid sequences SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, or 16;

2) the mature form of the polypeptides SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, or 16;

3) the polypeptides comprising the Cysteine-rich region of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, or 16;

4) the active variants of the amino acid sequence given by SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, or 16 wherein any amino acid specified in the chosen sequence is non-conservatively substituted, provided that no more than 15% of the amino acid residues in the sequence are so changed;

5) the active fragments, precursors, salts, or derivatives of the amino acid sequences given in 1) to 4);

6) a naturally occurring allelic variant of the sequence given by SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, or 16;

7) a naturally occurring allelic variant of the sequence given by SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, or 16, wherein the variant is the translation of a single nucleotide polymorphism;

8) a polypeptide of any of 1) to 7), wherein the polypeptide binds specifically an antibody or a binding protein generated against SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, or 16 or a fragment thereof;

9) a fusion protein comprising a polypeptide according to any of 1) to 8);

10) a fusion protein comprising a polypeptide according to any of 1) to 8), wherein said proteins further comprise one or more amino acid sequence belonging to these protein sequences: membrane-bound protein,

immunoglobulin constant region, multimerization domains, extracellular proteins, signal peptide-containing proteins, export signal-containing proteins;

11) a polypeptide encoded by a nucleic acid that hybridizes under high stringency conditions with a nucleic acid selected from the group consisting of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, or 15, or a complement of said DNA sequences or exhibits at least about 85% identity over a stretch of at least about 30 nucleotides, with a nucleic acid selected from the group consisting of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, or 15, or a complement of said DNA sequences;

b) an antagonist of a polypeptide of a1) to a8), wherein said antagonist comprises an amino acid sequence resulting from the modification of one or more residues of said polypeptide;

c) a ligand:

1) that binds specifically to a polypeptide according to any one of a1) to a8);

2) that binds specifically to a polypeptide according to any one of a1) to a8) and that antagonizes or inhibits the chemotactic activity of a polypeptide according to any one of a1) to a8);

3) which is a monoclonal antibody, a polyclonal antibody, a humanized antibody, an antigen binding fragment, or the extracellular domain of a membrane-bound protein;

d) an isolated nucleic acid:

1) encoding polypeptides of any of a1) to a8), said polypeptides having chemotactic activity;

2) encoding the fusion proteins of a9) or a10);

3) encoding the antagonists of b);

4) comprising a DNA sequence selected from the group consisting of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, or 15, or the complement of said DNA sequences;

5) that hybridizes under high stringency conditions with a nucleic acid selected from the group consisting of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, or 15, or a complement of said DNA sequences; or

6) exhibiting at least about 85% identity over a stretch of at least about 30 nucleotides, with a nucleic acid selected from the group consisting of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, or 15, or a complement of said DNA sequences;

e) a vector comprising a nucleic acid according to d);

f) a peptide mimetic designed on the sequence or the structure or both the sequence and structure of a polypeptide according to any one of a1) to a8);

g) a host cell transformed with a vector or a nucleic acid according to any of d) or e);

h) a primer comprising SEQ ID NO: 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28;

i) a compound that enhances the expression level of a polypeptide according to any one a1) to a8);

j) a compound that reduces the expression level of a polypeptide according to any one a1) to a8);

k) a pharmaceutical composition comprising any one of a) to j) and a pharmaceutically acceptable carrier;

l) a kit for measuring the activity and/or the presence of a chemokine-like polypeptide comprising one or more of the following reagents set forth in a) to k);

m) a transgenic animal cell that has been transformed with a vector or a nucleic acid according to d) or e), having constitutive or inducible altered expression levels of a polypeptide according to any one of a1) to a8); or

n) a transgenic non-human animal that has been transformed to have enhanced or reduced expression levels of a polypeptide according to a1) to a8).

43. The composition of matter of claim 42, wherein the nucleic acid molecule in said vector is operatively linked to expression control sequences allowing expression in prokaryotic or eukaryotic host cells of the encoded polypeptide.

44. The composition of matter of claim 42, wherein said polypeptides or ligands are in the form of active conjugates or complexes with a molecule chosen from radioactive labels, fluorescent labels, biotin, or cytotoxic agents.

45. The composition of matter of claim 42, wherein the compound that reduces the expression level of a polypeptide is an antisense oligonucleotide or a small interfering RNA.

46. A process for producing cells that produce a polypeptide comprising transforming a cell with a polynucleotide selected encoding SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, or 16 and culturing said cells to produce a polypeptide.

47. A method of using a composition of matter comprising obtaining a composition of matter according to claim 42 and using said composition of matter in a method selected from: making a genetically engineered cell; producing a polypeptide; producing a pharmaceutical composition; the treatment of a disease; screening candidate compounds; identifying a candidate compound; or determining the activity, presence or both activity or presence of said composition of matter.

48. The method of claim 47, comprising genetically engineering cells with composition of matter comprising a vector or a nucleic acid according to claim 42.

49. The method of claim 48, further comprising culturing said cell under conditions in which the nucleic acid or vector is expressed, and recovering the polypeptide encoded by said nucleic acid or vector from the culture.

50. The method of claim 47, comprising the administration of a therapeutically effective amount of a composition of matter comprising a polypeptide, a ligand, an antagonist, a peptide mimetic, a nucleic acid, a cell, or a compound as set forth in claim 42 to an individual for the treatment of a disease.

51. The method of claim 47, comprising a composition of matter comprising a polypeptide, a ligand, an antagonist, a peptide mimetic, a nucleic acid, a cell, or a compound as set forth in claim 42 with a pharmaceutically acceptable carrier to produce a pharmaceutical composition.

52. The method of claim 47, wherein said method screens for candidate compounds effective to treat a disease related to the chemokine-like polypeptides and comprises:

a) contacting a cell, a transgenic animal cell, or a transgenic non-human animal as set forth in claim 42 and having enhanced or reduced expression levels of the polypeptide with a candidate compound; and

b) determining the effect of the compound on the animal or on the cell.

53. The method of claim 47, wherein said method identifies a candidate compound as an antagonist/inhibitor or agonist/activator of a polypeptide of claim 42 and comprises:

a) contacting said polypeptide of claim 42, said compound, and a mammalian cell or a mammalian cell membrane capable of binding the polypeptide; and

b) measuring whether the molecule blocks or enhances the interaction of the polypeptide, or the response that results from such interaction, with the mammalian cell or the mammalian cell membrane.

54. The method of claim 47, said method determining the activity and/or the presence of a polypeptide in a sample, the method comprising:

a) providing a protein-containing sample;

b) contacting said sample with a ligand of claim 1; and

c) determining the presence of said ligand bound to said polypeptide.

55. The method of claim 47, said method determining the presence or the amount of a transcript or of a nucleic acid encoding a polypeptide and comprising:

a) providing a nucleic acid-containing sample;

b) contacting said sample with a nucleic acid of claim 42; and

c) determining the hybridization of said nucleic acid with a nucleic acid into the sample.

56. The method of claim 55, wherein said contacting comprises the use of the primer sequences comprising SEQ ID NO: 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27 or 28 for determining the presence or the amount of a transcript or of a nucleic acid encoding the polypeptide.

57. The method of claim 56, wherein the amount of said transcript or nucleic acid is determined by Polymerase Chain Reaction.